st96042sqlt.ST25
SEQUENCE LISTING

<110> ICARD-DICHKAERE, Christine
MALLET, Jacques
RAVASSARD, Philippe

<120> POLYPEPTIDES OF THE "BASIC-HELIX-LOOP-HELIX" bHLH FAMILY, CORRESPONDING NUCLEIC ACID
SEQUENCES

<130> ST96042AUS

<140> 09/595,947
<141> 2000-06-16

<150> FR96/15651
<151> 1996-12-19

<150> PCT/FR97/02368
<151> 1997-12-19

<150> US09/331,356
<151> 1997-12-19

<160> 28

<170> PatentIn version 3.0

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<213> Rattus norvegicus

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cgattagcag ctcagaagtc cctctgggtc tcaccactgc acagaggccg aggacccccct    180

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caaaacttcg aagcgagcag aggggttcag ctatccaccg ctgcttgact ctgaccaccc     300

gcagctctct gttctttttga gcccggagta actaggtaac atttaggaac ctccaaaggg    360

tagaagaggg gagtgggtgg gcgtactcta gtcccgcgtg gagtgacctc taagtcagag     420

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cgcccaccat ccaagtgtcc caagagaccc agcaacccttt ccccggagcc tcggaccacg    540

aagtgctcag ttccaattcc accccaccta gccccactct cgtaccgagg gactgctccg     600

aagcagaagc aggtgactgc cgagggacat cgaggaagct ccgtgcgcgg cgcggagggc     660

gcaacaggcc caagagcgag ttggcactga gcaagcagcg acgaagccgg cgcaagaagg     720

ccaacgaccg ggagcgcaac cgcatgcaca accttaactc cgcgctggat gcgctgcgcg     780

gtgtcctgcc caccttcccg gatgacgcca aacttacaaa gatcgagacc ctgcgcttcg     840

cccacaacta catttgggca ctgactcaga cgctgcgcat agcggaccac agcttctacg     900

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tggaggagtt ccctggcctg caggtgccca gctccccatc ctgtctgctc ccgggcaccc   1080

tggtgttctc agacttcttg tgaagggccc aaacaggccc tgggcggtgg gcgctggcag   1140

aaagggaggg agtcagagct gtctgaaatg gaaggtagtg gaggcactcg agcatctcgc   1200

cccttctggc tttcattagt caggtccctg atttaaccag gattcgcaca gttccttgct   1260

gctgtgcgtg cacaaaggac attgcaggct gatctcctct taaccctcct cagtgtggcc   1320

acctcaaact cccgctccaa gcagaggaga gccgtagcac taaatagttg ggagactccc   1380

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<213>  Rattus norvegicus

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Asn Ser Thr Pro Pro Ser Pro Thr Leu Val Pro Arg Asp Cys Ser Glu
        35                  40                  45

Ala Glu Ala Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg
    50                  55                  60

Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
65                  70                  75                  80

Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
                85                  90                  95

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His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
        100             105             110

Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
        115             120             125

His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
    130             135             140

Ser Phe Tyr Gly Pro Glu Pro Pro Val Pro Cys Gly Glu Leu Gly Ser
145             150             155             160

Pro Gly Gly Gly Ser Ser Gly Asp Trp Gly Ser Ile Tyr Ser Pro Val
            165             170             175

Ser Gln Ala Gly Ser Leu Ser Pro Thr Ala Ser Leu Glu Glu Phe Pro
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gacgggcagg ggaaagaggg atcctctgac ccagcggggg ctgggaggat ggctgttttt     240

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acccgtgaga cggagcggtc cttccccaga gcctcggaag acgaagtgac ctgccccacg     420

tccgccccgc ccagccccac tcgcacaccg gggaactgcg cagaggcgga agagggaggc     480

tgccgagggg ccccgaggaa gctccgggca cggcgcgggg gacgcagccg gcctaagagc     540

gagttggcac tgagcaagca gcgacggagt cggcgaaaga aggccaacga ccgcgagcgc     600

aatcgaatgc acgacctcaa ctcggcactg gacgccctgc gcggtgtcct gcccaccttc     660

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ccgcactgcg gggagctggg cagcccaggc ggtccccccg gggactgggg gtccctctac     840

tccccagtct cccaggctgg cagcctgagt cccgccgcgt cgctggagga gcgacccggg     900

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gcattgcaaa gtgcgctcat tttaggcctc ctctctgcca ccaccccata atcccattca   1260

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Thr Ser Ala Pro Pro Ser Pro Thr Arg Thr Pro Gly Asn Cys Ala Glu
        35                  40                  45

Ala Glu Glu Gly Gly Cys Arg Gly Ala Pro Arg Lys Leu Arg Ala Arg
    50                  55                  60

Arg Gly Gly Arg Ser Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
65                  70                  75                  80

Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
            85                  90                  95

His Asp Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
            100                 105                 110

Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
            115                 120                 125

His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
    130                 135                 140

Ser Leu Tyr Ala Leu Glu Pro Pro Ala Pro His Cys Gly Glu Leu Gly
145                 150                 155                 160

Ser Pro Gly Gly Pro Pro Gly Asp Trp Gly Ser Leu Tyr Ser Pro Val
                165                 170                 175

Ser Gln Ala Gly Ser Leu Ser Pro Ala Ala Ser Leu Glu Glu Arg Pro
            180                 185                 190

Gly Leu Leu Gly Ala Thr Ser Ser Ala Cys Leu Ser Pro Gly Ser Leu
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Ala Phe Ser Asp Phe Leu
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gaaugaaccc agccuaccgc ccccguggag gccugggccg gccaggdguc agcuagggag     300

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gcucccuccc ucucccuuac ccuuagcacc cacagcccag cgacagacag guccuuucac     420

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cgaccgcgag cgcaaucgaa ugcacgaccu caacucggca cuggacgccc ugcgcggugu     720

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